

TTGTAACAGA AAATTAAAT ATACTCCACT CAAGGGAATT CTGTACTTTG CCCTTTGGT -99  
 AAAGTCTCAT TTACATTCT AAACCTTCT TAAGAAATC GAATTCCTT TGATCTCT -39

1

-1 M T S C H I

TCTGAATTGC AGAAATCAGA TAAAACTAC TTGGTGAA ATG ACT TCT TGT CAC ATT 18

7 A E E H I Q K V A I F G G T H G

GCT GAA GAA CAT ATA CAA AAG GTT GCT ATC TTT GGA GGA ACC CAT GGG 66

23 N E L T G V F L V K H W L E N G

AAT GAG CTA ACC GGA GTA TTT CTG GTT AAG CAT TGG CTA GAG AAT GGC 114

39 A E I Q R T G L E V K P F I T N

GCT GAG ATT CAG AGA ACA GGG CTG GAG GTA AAA CCA TTT ATT ACT AAC 162

55 P R A V K K C T R Y I D C D L N

CCC AGA GCA GTG AAG AAG TGT ACC AGA TAT ATT GAC TGT GAC CTG AAT 210

71 R I F D L E N L G K K M S E D L

CGC ATT TTT GAC CTT GAA AAT CTT GGC AAA AAA ATG TCA GAA GAT TTG 258

87 P Y E V R R A Q E I N H L F G P

CCA TAT GAA GTG AGA AGG GCT CAA GAA ATA AAT CAT TTA TTT GGT CCA 306

103 K D S E D S Y D I I F D L H N<sup>\*</sup> T

AAA GAC AGT GAA GAT TCC TAT GAC ATT ATT TTT GAC CTT CAC AAC ACC 354

119 T S N M G C T L I L E D S R N N

ACC TCT AAC ATG GGG TGC ACT CTT ATT CTT GAG GAT TCC AGG AAT AAC 402

135 F L I Q M F H Y I K T S L A P L

TTT TTA ATT CAG ATG TTT CAT TAC ATT AAG ACT TCT CTG GCT CCA CTA 450

151 P C Y V Y L I E H P S L K Y A T

CCC TGC TAC GTT TAT CTG ATT GAG CAT CCT TCC CTC AAA TAT GCG ACC 498

167 T R S I A K Y P V G I E V G P Q

FIG.1A



183 ACT CGT TCC ATA GCC AAG TAT CCT GTG GGT ATA GAA GTT GGT CCT CAG 546  
 P Q G V L R A D I L D Q M R K M  
 CCT CAA GGG GTT CTG AGA GCT GAT ATC TTG GAT CAA ATG AGA AAA ATG 594  
 199 I K H A L D F I H H F N E G K E  
 ATT AAA CAT GCT CTT GAT TTT ATA CAT CAT TTC AAT GAA GGA AAA GAA 642  
 215 F P P C A I E V Y K I I E K V D  
 TTT CCT CCC TGC GCC ATT GAG GTC TAT AAA ATT ATA GAG AAA GTT GAT 690  
 231 Y P R D E N G E I A A I I H P N  
 TAC CCC CGG GAT GAA AAT GGA GAA ATT GCT ATC CAT CAT CCT AAT 738  
 247 L Q D Q D W K P L H P G D P M F  
 CTG CAG GAT CAA GAC TGG AAA CCA CTG CAT CCT GGG GAT CCC ATG TTT 786  
 263 L T L D G K T I P L G G D C T V  
 TTA ACT CTT GAT GGG AAG ACG ATC CCA CTG GGC GGA GAC TGT ACC GTG 834  
 279 Y P V F V N E A A Y Y E K K E A  
 TAC CCC GTG TTT GTG AAT GAG GCC GCA TAT TAC GAA AAG AAA GAA GCT 882  
 295 F A K T T K L T L N A K S I R C  
 TTT GCA AAG ACA ACT AAA CTA ACG CTC AAT GCA AAA AGT ATT CGC TGC 930  
 311 C L H  
 TGT TTA CAT TAG AA ATCACTTCCA GCTTACATCT TACACGGTGT CTTACAAATT 984  
 CTGCTAGTCT GTAAGTCTCT TAAGAGTAGG GTTGTGCTT ATTCAACTGC ATACATAGCT 1044  
 CCTAGCACAG TGCCTTATTC GGTAGGCATC TAAGCAAAAT TCTTAAATTA ATTAATATAT 1104  
 CTTTAAAGAT ATCATATTTT ATGTATGTAG CTTATTCAAA GAAGTGTTC CTATTTCTAT 1164  
 ATAGTTTTATT ATACATGATA CTTGGGTAGC TCAACATTCT TATTAACAG CCTTTGTATT 1224  
 CAGAATATAA AATTGAAATA GATATATATA AGTTAAAAA AAAAAAAA AAA 1277

FIG.1B

	10v	20v	30v	40v	50v
HLASP	MTSCHIAEEHIQKVAIFGGTHGNETGVFLVKHWLENGAEIQRTGLEVKPFP				
	MTSCH:AE: . I:KVAIFGGTHGNETGVFLVKHWLEN::EIQRTGLEVKPFP				
BASPCDNA	MTSCHVAEDPIKKVAIFGGTHGNETGVFLVKHWLENSTEIQRTGLEVKPFP				
	10^	20^	30^	40^	50^
	60v	70v	80v	90v	100v
HLASP	ITNPRAVKKCTRYIDCDLNRIFDLENLGKKMS <del>EDLPYEVRR</del> AEINHLFGP				
	ITNPRAVKKCTRYIDCDLNR:FD ENLGKK.SEDLPYEVRRAEINHLFGP				
BASPCDNA	ITNPRAVKKCTRYIDCDLNRVFDPENLGKKKS <del>EDLPYEVRR</del> AEINHLFGP				
	60^	70^	80^	90^	100^
	110v	120v	130v	140v	150v
HLASP	KDS <del>EDSYDII</del> FDLHN'TTSNMGCTLI <del>EDSRN</del> F <del>LIQM</del> FHYIKTS <del>SLAP</del> PCY				
	KDS <del>EDSYDII</del> FDLHN'TTSNMGCTLI <del>EDSRN</del> :FLI <del>QM</del> FHYIKTS <del>SLAP</del> PCY				
BASPCDNA	KDS <del>EDSYDII</del> FDLHN'TTSNMGCTLI <del>EDSRN</del> D <del>FLIQM</del> FHYIKTS <del>SLAP</del> PCY				
	110^	120^	130^	140^	150^
	160v	170v	180v	190v	200v
HLASP	VYLIEHPSLKYATTRSIAKYPVGIEVGPQPGVLRADILDQMRMKIHALD				
	VYLIEHPSLKYATTRSIAKYPVGIEVGPQPGVLRADILDQMRKMI:HALD				
BASPCDNA	VYLIEHPSLKYATTRSIAKYPVGIEVGPQPGVLRADILDQMRMKIQHALD				
	160^	170^	180^	190^	200^
	210v	220v	230v	240v	250v
HLASP	FIHHFN <del>EGKEFP</del> PPCAIEVYKII <del>EKVDYPR</del> DENGEIAAIIHPNLQDQDWKPL				
	FIH:F <del>NEGKEFP</del> PPCAIEVYKI: KVDYPR:E:GEI:AIHP:LQDQDWKPL				
BASPCDNA	FIHHFN <del>EGKEFP</del> PPCAIEVYKIMRKVDYPRNESGEISAIHPKLQDQDWKPL				
	210^	220^	230^	240^	250^
	260v	270v	280v	290v	300v
HLASP	HPGDPMFL <del>TLDGKTI</del> PLGG <del>CTVYPVFVNEAAYE</del> KK <del>EAF</del> AKTTKLT <del>LN</del> AK				
	HP.DP:FL <del>TLDGKTI</del> PLGG TVYPVFVNEAAYEKK <del>EAF</del> AKTTKLT <del>LN</del> A:				
BASPCDNA	HPEDPVFL <del>TLDGKTI</del> PLGG <del>CTVYPVFVNEAAYE</del> KK <del>EAF</del> AKTTKLT <del>LN</del> AN				
	260^	270^	280^	290^	300^
	310v				
HLASP	SIRCC <del>LH</del>				
	SIR..LH				
BASPCDNA	SIRSS <del>LH</del>				
	310^				

FIG. 2

BEST AVAILABLE COPY

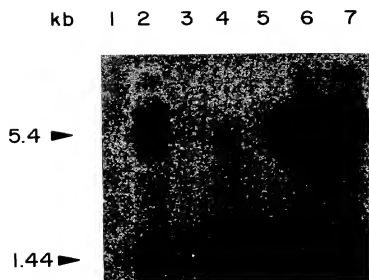


FIG. 3

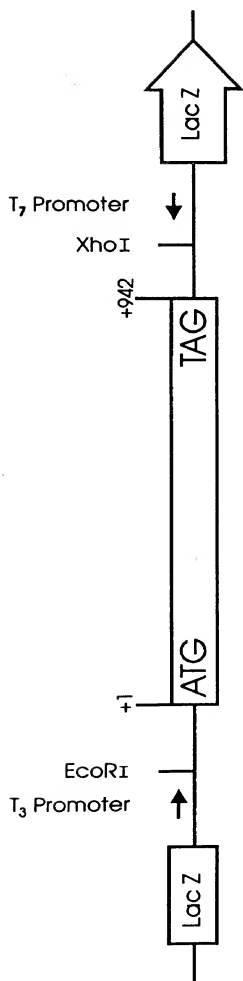


FIG. 4

FIG.5A

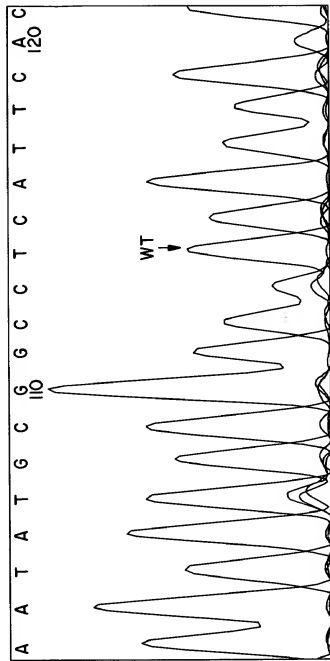


FIG.5B

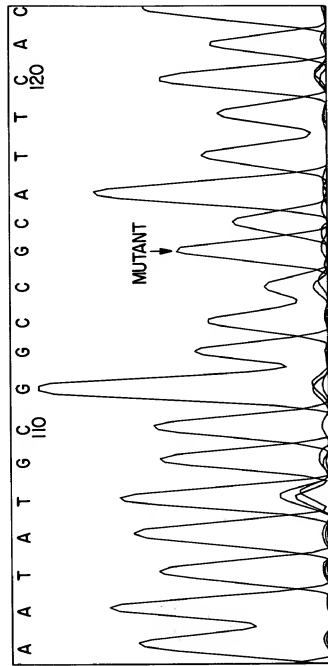


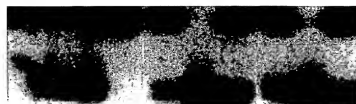


FIG.6A



▶ WT  
 ▶ MUT  
 ▶ WT  
 ▶ MUT

FIG.6B



▶ 239 bp  
 ▶ 125 bp  
 ▶ 114 bp

EAM		M	E	M	N	DSNDSBB
ASA		B	C	N	L	STCSESS
MPE		O	5	L	A	AYOACAA
1E3		2	7	1	4	11111JJ

/  
 ATGACTTCTTGTACATTGCTGAAGAACATATACAAAAGGTTGCTATCTTTGGAGGAACC  
 TACTGAAGAACAGTGTAACGACTTCTTGATATGTTTTCACGATAGAAACCTCCTTGG

60

m t s c h i a e e h i q k v a i f g g t  
 ↑ START SITE

N A BBH TSM ✓ RM H HHD TH  
 L L SCP RPS MA I HAD FN  
 A U AAA UOE AE N AEE IF  
 3 1 W72 911 11 P 121 11

//  
 CATGGGAATGAGCTAACCGGAGTATTTCTGGTTAAGCATTGGCTAGAGAATGGCGCTGAG  
 GTACCCTTACTCGATTGGCCTCATAAAGACCAATTCGTAACCGATCTCTTACCGCGACTC

120

h g n e l t g v f l v k h w l e n g a e

M B  
 N P  
 L M  
 1 1

ATTCAGAGAACAGGGCTGGAGGTAAAACCATTTATTACTAACCCACAGAGCAGTGAAGAAG  
 TAAGTCTCTTGTCCCGACCTCCATTTTGGTAAATAATGATTGGGGTCTCGTCACTTCTTC

180

i q r t g l e v k p f i t n p r a v k k

FIG. 7(a)





MN A	HBN M	TH E AS	TM
NL P	GSS N	FN C PC	RS
LA L	IIP L	IF R YR	UE
13 1	AH2 1	11 2 11	91
/	//	/	↓

AACATGGGGTGCACCTCTTATTCTTGAGGATTCCAGGAATAACTTTTAAATTCAGATGTTT 420

TTGTACCCACGTGAGAATAAGAACTCCTAAGGTCCTTATGAAAAATTAAGTCTACAAA

n m g c t l i l e d s r n n f l i q m f

TM	N	M F	E
RS	L	A O	C
UE	A	E K	O
91	4	2 1	B

↓

CATTACATTAAGACTTCTCTGGCTCCACTACCCTGCTACGTTTATCTGATTGAGCATCCT 480

GTAATGTAATTCTGAAGAGACCGAGGTGATGGGACGATGCAAATAGACTAACTCGTAGGA

h y i k t s l a p l p c y v y l i e h p

S	M	A
F	N	V
A	L	A
N	1	2

TCCTCAAATATGCGACCACTCGTTCCATAGCCAAGTATCCTGTGGGTATAGAAGTTGGT 540

AGGGAGTTTATACGCTGGTGAGCAAGGTATCGGTTTCATAGGACACCCATATCTCAACCA

s l k y a t t r s i a k y p v g i e v g

FIG. 7(c)

D	M	M D	A	E	BMDD	TM
D	N	N D	L	C	IBPP	RS
E	L	L E	U	R	NONN	UE
1	1	1 1	1	V	1121	91

CCTCAGCCTCAAGGGGTTCTGAGAGCTGATATCTTGGATCAAATGAGAAAAATGATTAAA  
 GGAGTCGGAGTTCCCCAAGACTCTCGACTATAGAACCTAGTTTACTCTTTTACTAATTT  
 p q p q g v l r a d i l d q m r k m i k

NN	HMHM
SL	INHN
PA	NLAL
H3	P111

CATGCTCTTGATTTTATACATCATTTCAATGAAGGAAAAGAATTTCCCTCCCTGCGCCATT  
 GTACGAGAACTAAATATGTAGTAAAGTTACTTCCTTTTCTTAAAGGAGGGACGCGGTAA  
 h a l d f i h h f n e g k e f p p c a i

E	BSBNXSASSBBHNSB	FF	F	IF
C	SESCMMVCESSPCCB	OO	O	TN
P	ACAIAAAARCAAAIRV	KK	K	AU
1	J1J111111J2111	11	1	1H

GAGGTCTATAAAATTATAGAGAAAGTTGATTACCCCGGGATGAAAATGGAGAAATTGCT  
 CTCCAGATATTTTAATATCTCTTTCAACTAATGGGGGCCCTACTTTTACCTCTTTAACGA  
 e v y k i i e k v d y p r d e n g e i a

c693>d  
 Y231>X

FIG. 7(d)

S	PBMD	F	ESASBBSBXBNMDD
F	SIBPP	O	CEPCSSFIHALBPPI
C	TNONN	K	RCYRAAANOMAONNN
1	11121	1	2111JJN12141211

GCTATCATCCATCCTAATCTGCAGGATCAAGACTGGAAACCACTGCATCCTGGGGATCCC  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 CGATAGTAGGTAGGATTAGACGTCCTAGTTCTGACCTTTGGTGACGTAGGACCCCTAGGG 780  
 a i i h p n l q d q d w k p l h p g d p  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  

N	TM	B	MDBBBDBMA	BBAB	CR	CR
L	RS	B	BPBSPPIBL	SSCS	SS	SS
A	UE	V	ONSCUNNOW	ILIM	PA	PA
3	91	2	121911122	Y112	61	61

ATGTTTTTAACTCTTGATGGGAAGACGATCCCACTGGCGGGAGACTGTACCGTGTACCCC  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 TACAAAAATGAGAACTACCCTTCTGCTAGGGTGACCCGCTCTGACATGGCACATGGGG 840  
 m f l t l d g k t i p l g g d c t v y p  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  

SM	HIFA	H A
PN	ATNC	I L
OL	EAUI	N U
11	31H1	3 1

GTGTTTGTGAATGAGGCCGCATATTACGAAAAGAAAGAAGCTTTTGCAAAGACAATAAA  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 CACAAAACACTTACTCCGGCGTATAATGCTTTTCTTTCTTCGAAAACGTTTCTGTTGATT 900  
 v f v n e a a y y e k k e a f a k t t k  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+

a854>c  
 E285>A

FIG. 7(e)

S	B	HIF	E	A
P	B	NTN	C	L
O	V	FAU	1	U
1	1	31H	5	1

CTAACGCTCAATGCAAAAAGTATTTCGCTGCTGTTTACATTAGAAATCACCTCCAGCTTAC  
 GATTGCGAGTTACGTTTTTCATAAGCGACGACAAATGTAATCTTTAGTGAAGGTCGAATG  
 1 t l n a k s i r c c l h . k s l p a y  
 RM A ATM  
 MA L FRS  
 AE U LUE  
 11 1 291  
 ATCTTACACGGTGCTCTTACAAATTCTGCTAGTCTGTAAGCTCCCTTAAGAGTAGGGTTGTG  
 TAGAATGTGCCACAGAATGTTTAAGACGATCAGACATTCGAGGAATTCTCATCCCAACAC  
 i l h g v l q i l l v c k l l k s r v v  
 B A RM H D S  
 S L MA N D F  
 P U AE F E A  
 W 1 11 3 1 N  
 CCTTATTCAACTGCATACATAGTCTCCTAGCACAGTGCTTATTTCGGTAGGCATCTAAGCA  
 GGAATAAGTTGACGTATGTATCGAGGATCGTGTCACGGAATAAGCCATCCGTAGATTCTGT  
 p y s t a y i a p s t v p y s v g i . a

FIG.7(f)

✓ TM	✓ RS	✓ UE	✓ 91	ATM SRS EUE	PATM ASRS CEUE	191 1191	✓ TDM	✓ RRS	✓ UAE	✓ 911	E C R V	A L U 1
---------	---------	---------	---------	-------------------	----------------------	-------------	----------	----------	----------	----------	------------------	------------------

/   /   /   /  
 AATTTCTTAAATTAATTAATATATCTTTAAAGATATCATATTTTATGTATGTAGCTTATT  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+  
 TTAAAGAATTTAATTAAATTATATAGAAATTTCTATAGTATAAAATACATACATCGAATAA

1140

n f l n . l i y l . r y h i l c m . l i  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+

X	N	A
M	L	L
N	A	U
1	3	1

CAAAGAAGTGTTCCTATTCTATATAGTTTATTATACATGATACTTGGGTAGCTCAACA  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+  
 GTTCTCTCACAAAGGATAAAGATATATCAAATAATATGTACTATGAACCCATCGAGTTGT  
 q r s v s y f y i v y y t . y l g s s t

1200

-----+-----+-----+-----+-----+-----+-----+-----+-----+

✓ TM	✓ RS	✓ UE	✓ 91		✓ TM	✓ RS	✓ UE	✓ 91
---------	---------	---------	---------	--	---------	---------	---------	---------

/   /  
 TTCTTAATAAACAGCCTTTGTATTGAGAATATAAAATTGAAATAGATATATATAAAGTTA  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+  
 AAGAATTATTTGTCGGAACATAAGTCTTATATTTTAACTTTATCTATATATATTTCAAT

1260

f l i n s l c i q n i k l k . i y i k l  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+

AAAAAAAAAAAAAAAAAA  
 -----+-----+-----+-----+-----+-----+-----+-----+-----+  
 TTTTTTTTTTTTTTTT  
 k k k k k k

1277

-----+-----+-----+-----+-----+-----+-----+-----+-----+

FIG. 7(g)

v-21 v-1  
TCTTCTGAAT TGCAGAAATC AGATAAAAAC TACTTGGTGA

v19  
A ATG ACT TCT TGT CAC ATT GCT GAA GAA CAT ATA CAA  
Met Thr Ser Cys His Ile Ala Glu Glu His Ile Gln  
^3 ^6 ^9 ^12

v39 v59  
AAG GTT GCT ATC TTT GGA GGA ACC CAT GGG AAT GAG  
Lys Val Ala Ile Phe Gly Gly Thr His Gly Asn Glu  
^15 ^18 ^21 ^24

v79 v99  
CTA ACC GGA GTA TTT CTG GTT AAG CAT TGG CTA GAG  
Leu Thr Gly Val Phe Leu Val Lys His Trp Leu Glu  
^27 ^30 ^33 ^36

v119 v139  
AAT GGC GCT GAG ATT CAG AGA ACA GGG CTG GAG GTA  
Asn Gly Ala Glu Ile Gln Arg Thr Gly Leu Glu Val  
^39 ^42 ^45 ^48

v159  
AAA CCA TTT ATT ACT AAC CCC AGA GCA GTG AAG AAG  
Lys Pro Phe Ile Thr Asn Pro Arg Ala Val Lys Lys  
^51 ^54 ^57 ^60

v199  
TGT ACC AGA TAT ATT GAC TGT GAC CTG AAT CGC ATT  
Cys Thr Arg Tyr Ile Asp Cys Asp Leu Asn Arg Ile  
^63 ^66 ^69 ^72

v219 v239  
TTT GAC CTT GAA AAC CTT GG GTAAGACTA-TGCTTTGTAT  
Phe Asp Leu Glu Asn Leu Gly  
^75 ^78

v259 v279  
TGTATATCTA TCGATCTTCT GTCAAAGTGG TAGGTCTGT

FIG. 8

v-42	v-32	v-22	v-12
TATTATCTCA GGCACAGATG TTGTTCTCT TTTCTTTCT			
v-2	v8	v18	
GCTTATAACA G	C AAA AAA ATG TCA GAA GAT TTG CCA TAT		
	Lys Lys Met Ser Glu Asp Leu Pro Tyr		
	^80		
v28	v38	v48	v58
GAA GTG AGA AGG GCT CAA GAA ATA AAT CAT TTA TTT			
Glu Val Arg Arg Ala Gln Glu Ile Asn His Leu Phe			
v68	v78	v88	v98
GGT CCA AAA GAC AGT GAA GAT TCC TAT GAC ATT ATT			
Gly Pro Lys Asp Ser Glu Asp Ser Tyr Asp Ile Ile			
v108	v118	v128	
TTT GAC CTT CAC AAC ACC ACC TCT AAC ATG GGG TGC			
Phe Asp Leu His Asn Thr Thr Ser Asn Met Gly Cys			
v138	v148	v158	v168
ACT CTT ATT CTT GAG GAT TCC AGG AAT AAC TTT TTA			
Thr Leu Ile Leu Glu Asp Ser Arg Asn Asn Phe Leu			
v178	v188	v198	
ATT CAG ATG TTT CAT TAC ATT AAG	GTAATGTT		
Ile Gln Met Phe His Tyr Ile Lys			
	^144		
v208	v218	v228	
AATGTTATTA ATTTATAAGT CAGCAAAGCA CTTC			

FIG. 9



v-37                      v-27                      v-17                      v-7  
**AACATACGGC TTTTACCCA AGAAAGACGT TTTTGATTTT**

v3                      v13                      v23  
**TTTCAG** ACT TCT CTG GCT CCA CTA CCC TGC TAC GTT  
 Thr Ser Leu Ala Pro Leu Pro Cys Tyr Val  
                          ^3                      ^6                      ^9

v33                      v43                      v53                      v63  
 TAT CTG ATT GAG CAT CCT TCC CTC AAA TAT GCG ACC  
 Tyr Leu Ile Glu His Pro Ser Leu Lys Tyr Ala Thr  
                          ^12                      ^15                      ^18                      ^21

v73                      v83                      v93  
 ACT CGT TCC ATA GCC AAG TAT CCT GTG G **GTAA**  
 Thr Arg Ser Ile Ala Lys Tyr Pro Val  
                          ^24                      ^27                      ^30

v103                      v113                      v123                      v133  
**GTGATAGTTC CCACGTTCAT AACTCAATAA AATATGTCCT**

v143                      v153  
**ACCTGAAACT CAGACA**

FIG.10

	v-30		v-20		v-10	
	TACTTATATA AATGTGACTA TCTCTCCTTC TCTACCTAG					G
		v10		v20		v30
T	ATA	GAA	GTT	GGT	CCT	CAG
	Ile	Glu	Val	Gly	Pro	Gln
					Pro	Gln
					Gly	Val
					Leu	Arg
						^177
		v40		v50		v60
	GCT	GAT	ATC	TTG	GAT	CAA
	Ala	Asp	Ile	Leu	Asp	Gln
					Met	Arg
					Lys	Met
					Ile	Lys
		v80		v90		v100
	CAT	GCT	CTT	GAT	TTT	ATA
	His	Ala	Leu	Asp	Phe	Ile
					His	His
					Phe	Asn
					Glu	
						^211
		v120		v130		v140
	TAA	TAATGAAGGT		AACGTTATCA		AACTTAACCA
						CCAAACATT
		v160		v170		v180
	AAATAACAAAT		TCGAACCTGG		GTGAGA	

FIG. 11



v-65                      v-55                      v-45                      v-35  
GTCTAGAGCTC TGACATAAAT TTCTAGAGGA GAAAAACCAA

v-25                      v-15                      v-5                      v5  
ATATAATATA TTATTTTGA TTCTTCTCTG AGAG GAT CAA GAC  
 Asp Gln Asp  
 ^249

v15                      v25                      v35  
 TGG AAA CCA CTG CAT CCT GGG GAT CCC ATG TTT TTA  
 Trp Lys Pro Leu His Pro Gly Asp Pro Met Phe Leu

v45                      v55                      v65                      v75  
 ACT CTT GAT GGG AAG ACG ATC CCA CTG GGC GGA GAC  
 Thr Leu Asp Gly Lys Thr Ile Pro Leu Gly Gly Asp

v85                      v95                      v105  
 TGT ACC GTG TAC CCC GTG TTT GTG AAT GAG GCC GCA  
 Cys Thr Val Tyr Pro Val Phe Val Asn Glu Ala Ala

v125                      v135                      v145  
 TAT TAC GAA AAG AAA GAA GCT TTT GCA AAG ACA ACT  
 Tyr Tyr Glu Lys Lys Glu Ala Phe Ala Lys Thr Thr

v155                      v165                      v175                      v185  
 AAA CTA ACG CTC AAT GCA AAA AGT ATT CGC TGC TGT  
 Lys Leu Thr Leu Asn Ala Lys Ser Ile Arg Cys Cys

v195                      v205                      v215  
 TTA CAT **TAG** AAATCA CTTCCAGCTT ACATCTTACA  
 Leu His **ter**  
 ^313

v225                      v235                      v245                      v255  
 CCGGTGCTCTTA CAAATTCTGC TAGTCTGTAA GCTCCTTAAG

v265  
 AGTAGGGTT

FIG.13